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M A S A G G E D C E S P A P E A																			16	SEQ ID NO:2
GAGCGGAGGCCGAG ATG GCT TCG GCG GGA GGC GAA GAC TGC GAG AGC CCC GCG CCG GAG GCC																			48	
↑SEQ ID NO:3→																				
D R P H Q R P F L I G V S G G T A S G K																			36	
GAC CGT CCG CAC CAG CGG CCC TTC CTG ATA GGG GTG AGC GGC GGC ACT GCC AGC GGG AAG																			108	
S T V C E K I M E L L G Q N E V E Q R Q																			56	
TCG ACC GTG TGT GAG AAG ATC ATG GAG TTG CTG GGA CAG AAC GAG GTG GAA CAG CGG CAG																			168	
R K V V I L S Q D R F Y K V L T A E Q K																			76	
CGG AAG GTG GTC ATC CTG AGC CAG GAC AGG TTC TAC AAG GTC CTG ACG GCA GAG CAG AAG																			228	
A K A L K G Q Y N F D H P D A F D N D L																			96	
GCC AAG GCC TTG AAA GGA CAG TAC AAT TTT GAC CAT CCA GAT GCC TTT GAT AAT GAT TTG																			288	
M H R T L K N I V E G K T V E V P T Y D																			116	
ATG CAC AGG ACT CTG AAG AAC ATC GTG GAG GGC AAA ACG GTG GAG GTG CCG ACC TAT GAT																			348	
F V T H S R L P E T T V V Y P A D V V L																			136	
TTT GTG ACA CAC TCA AGG TTA CCA GAG ACC ACG GTG GTC TAC CCT GCG GAC GTG GTT CTG																			408	
F E G I L V F Y S Q E I R D M F H L R L																			156	
TTT GAG GGC ATC TTG GTG TTC TAC AGC CAG GAG ATC CGG GAC ATG TTC CAC CTG CGC CTC																			468	
F V D T D S D V R L S R R V L R D V R R																			176	
TTC GTG GAC ACC GAC TCC GAC GTC AGG CTG TCT CGA AGA GTT CTC CGG GAC GTG CGC CGA																			528	
G R D L E Q I L T Q Y T T F V K P A F E																			196	
GGG AGG GAC CTG GAG CAG ATT CTG ACG CAG TAC ACC ACC TTC GTG AAG CCG GCC TTC GAG																			588	
E F C L P T K K Y A D V I I P R G V D N																			216	
GAG TTC TGC CTG CCG ACA AAG AAG TAT GCC GAT GTG ATC ATC CCA CGA GGA GTG GAC AAT																			648	
M V A I N L I V Q H I Q D I L N G D I C																			236	
ATG GTT GCC ATC AAC CTG ATC GTG CAG CAC ATC CAG GAC ATT CTG AAT GGT GAC ATC TGC																			708	
K W H R G G S N G R S Y K R T F S E P G																			256	
AAA TGG CAC CGA GGA GGG TCC AAT GGG CGG AGC TAC AAG CGG ACC TTT TCT GAG CCA GGG																			768	
D H P G M L T S G K R S H L E S S S R P																			276	
GAC CAC CCT GGG ATG CTG ACC TCT GGC AAA CGG TCA CAT TTG GAG TCC AGC AGC AGA CCC																			828	
H *																			278	
CAC TGA																			834	
↓SEQ ID NO:3↑																				
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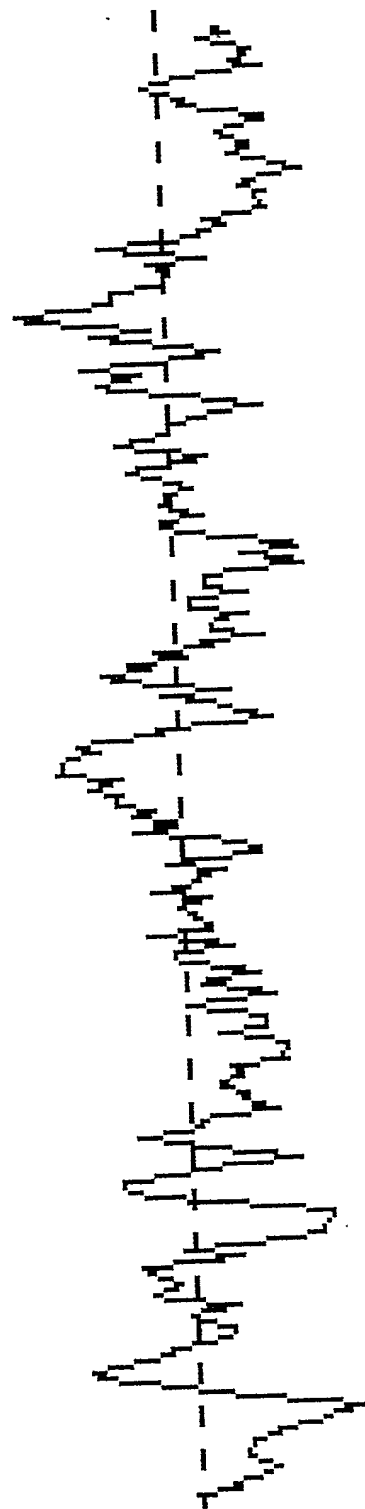
FIGURE 1a

GGGGAAATTGAGGAGACAGCCTAGACACTGGCTGGCCTGATGTTTTGTTGACAGTGAACCCACAGTGGGAGAGAGTTTT  
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TTACATGTCCTCATGTTTTCTGTTTTCTGTTTCATAACACAAGGCTGGTTGTGGCCTACAAACCTAA.TTCATGACCCA  
GTGGTTTGCAGTCCAGCGTGGCCTACACGGATATGGGGAGCCACTGAGGGATGTTTTCCCCCCTTGCTTGTGCCTTAAA  
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FIGURE 1b

103290" 22595860

PFAH



CR5

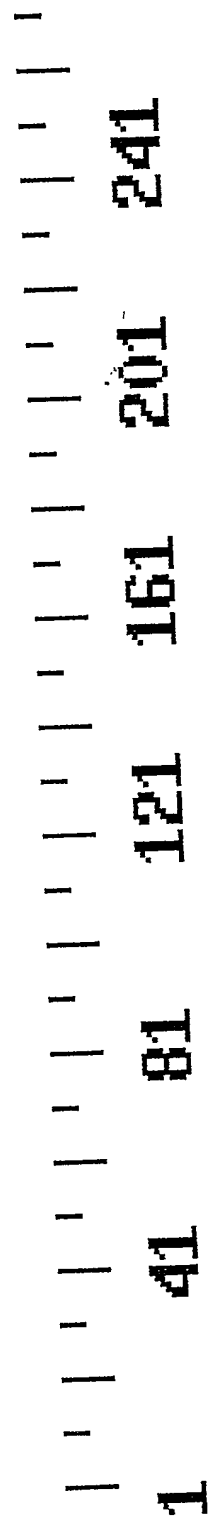


FIGURE 2

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*->vIGVaGsSGaGKtTvarrivsifgregvpaagiEGnpDsNtgdsflr      SEQ ID NO:4
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25  LIGVSGGTASGKSTVCEKIMELLGQNEVE-----QRQRKVIVLS 63

ldrifymdlhledrkragnkhysffsPeAndFDLLyevfkeLkeGksvdkP
drfy++l++e+++ a + +y+f+ P A+d DL+ +++k+ eGk+v++P
64 QDRFYKVLTAEQAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP 113

iYnHvtgerdpdgqePGtFTdwpeliegadvLviEGLHalyDerevNvaq
+Y++vt++r p      ++ +++++adv+ +EG++ +Y      +++
114 TYDFVTHSRLP-----ETTVVYPADVVLFEgilVFYSQE---IRD 150

LlDlkiyvDpdidlelarKiqRDmaERghslEgvlDsiekrrKPdyvNYI
l ++vD+d+d++l+r+ . RD+ RG++lE +l ++ +++KP+++ +
151 MFHLRLFVDTSDVRLSRRVLRDV-RRGRDLEQILTYTTFVKPAFEFEC 199

aPQfsyaDliiqrvtvdtsndFiakiipvrdele<-*
P+++yaD+ii+r+ ++ +++++ ++++++ d+l
200 LPTKKYADVIIIPRGVDNMVAIN--LIVQHIQDIL 231

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FIGURE 3

